



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Coughlin, Shaun R.
Ishihara, Hiroaki
Connolly, Andrew
 - (ii) TITLE OF INVENTION: Protease-Activated Receptor
3 and Uses Thereof
 - (iii) NUMBER OF SEQUENCES: 23
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MORRISON & FOERSTER
 - (B) STREET: 755 Page Mill Road
 - (C) CITY: Palo Alto
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94304-1018
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/208,629
 - (B) FILING DATE: 08-DEC-1998
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/742,440
 - (B) FILING DATE: 30-OCT-1996
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Catherine M. Polizzi
 - (B) REGISTRATION NUMBER: 40,130
 - (C) REFERENCE/DOCKET NUMBER: 220002060310
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (650) 813-5600
 - (B) TELEFAX: (650) 494-0792
 - (C) TELEX: 706141
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1224 base pairs
 - (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGACTTTGTA	TACTTAACAA	CATCCTGTAG	CCGGGTCTCA	GGACATCAAG	ATGAAAATCC	60
TTATCTTGGT	TGCAGCTGGG	CTGCTGTTTC	TGCCAGTCAC	TGTTTGCCAA	AGTGGCATAA	120
ATGTTTCAGA	CAACTCAGCA	AAGCCAACCT	TAACATATTAA	GAGTTTTAAT	GGGGGTCCCC	180
AAAATACCTT	TGAAGAATTC	CCACTTTCTG	ACATAGAGGG	CTGGACAGGA	GCCACCACAA	240
CTATAAAAGC	GGAGTGTTCC	GAGGACAGTA	TTTCAACTCT	CCACGTGAAT	AATGCTACCA	300
TAGGATACCT	GAGAAGTTCC	TTAAGTACCC	AAGTGATACC	TGCCATCTAT	ATCCTGCTGT	360
TTGTGGTTGG	TGTACCATCC	AACATCGTGA	CCCTGTGGAA	ACTCTCCTTA	AGGACCAAAT	420
CCATCAGTCT	GGTCATCTTT	CACACCAACC	TGGCCATCGC	AGATCTCCTT	TTCTGTGTCA	480
CACTGCCATT	TAAGATCGCC	TACCATCTCA	ATGGCAACAA	CTGGGTATTT	GGCGAGGTCA	540
TGTGCCGGAT	CACCACGGTC	GTTTTCTACG	GCAACATGTA	CTGCGCTATC	CTGATCCTCA	600
CTTGCAATGG	CATCAACCGC	TACCTGGCCA	CGGCTCACCC	TTTCACATAC	CAGAAGCTGC	660
CCAAACGCAG	CTTCTCCTTG	CTCATGTGTG	GCATAGTGTG	GGTCATGGTT	TTCTTATACA	720
TGCTGCCCTT	TGTCATCCTG	AAGCAGGAGT	ACCACCTCGT	CCACTCAGAG	ATCACCACCT	780
GCCACGATGT	CGTCGACGCG	TGCGAGTCCC	CATCATCCTT	CCGATTCTAC	TACTTCGTCT	840
CCTTAGCATT	CTTTGGGTTC	CTCATCCCCT	TTGTGATCAT	CATCTTCTGT	TACACGACTC	900
TCATCCACAA	ACTTAAATCA	AAGGATCGGA	TATGGCTGGG	CTACATCAAG	GCCGTCTCTC	960
TCATCCTTGT	GATTTTCACA	ATTTGCTTTG	CCCCACCAA	CATCATACTC	GTAATCCACC	1020
ATGCCAACTA	CTACTACCAC	AATACCGACA	GCTTGTAATT	TATGTATCTT	ATTGCTCTGT	1080
GCCTGGGGAG	CCTGAATAGC	TGCCTAGATC	CATTCTTTTA	CTTTGTCTATG	TCGAAAGTTG	1140
TAGATCAGCT	TAATCCTTAG	TCGGCAATGG	CAAGACCACT	TTAGAGACCA	AGGAGAGATA	1200
TCTGGGAAGA	CATACATGCT	TGGC				1224

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..124
(D) OTHER INFORMATION: n= A, T, C, or G

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCATATGCTA	ATATTTCTCT	TCAATTACAG	GCATAAATGT	TTCAGACAAC	TCAGCAAAGC	60
CAACCTTAAC	TATTAAGAGT	TTTAATGGGG	GTCCCCAAAA	TACCTTTGAA	GAATTCNNNN	120
NNNTACAAC	CTCCATGTGA	ATAATGCTAC	CATGGGATAC	CTGAGAAGTT	CCTTAAGTAC	180
CAAAGTGATA	CCTGCCATCT	ACATCCTGGT	GTTTGTGATT	GGTGTACCAG	CGAACATCGT	240
GACCCTGTGG	AAACTCTCCT	CAAGGACCAA	ATCCATCTGT	CTGGTCATCT	TTACACCAA	300
CCTGGCCATC	GCGGATCTCC	TTTTCTGTGT	CACGCTGCCG	TTTAAGATCN	NCCTACCATC	360
TCAATGGCAA	CAACTGGGTA	TTTGGCGAGG	TCATGTGCCG	GATCACCACG	GTCGTTTTCT	420
ACGGCAACAT	GTACTGCGCT	ANNNTCCTGA	TCCTCACCTG	CATGGGCATC	AACCGCTACC	480
TGGCCACGGC	TCACCCTTTT	ACATACCAGA	AGCTGCCCAA	ACGCAGCTTC	TCCATGCTCA	540
TGTGTGGCAT	GGTGTGGGTC	ATGGTTTTCT	TATACATGCT	GCCCTTTGTC	ATCCNNNAAG	600

CAGGAGTACC	ACCTCGTCCA	CTCCGAGATC	ACCACCTGCC	ACGATGTCGT	CGACGCGTGC	660
GANTCCCCAT	CATCCTTCCG	ATTCTACTAC	TTCGTCTCCT	TAGCATTCCT	TGGGTTTCCTC	720
ATCCCGTTTG	TGATCATCAT	CTTCTGTTAC	ACGACTCTCA	TCCACAAACT	TAAATCAAAA	780
GATCNGATAT	GGCTGGGCTA	CATCAAGGCC	GTCCTCCTCA	TCCTTGTTGAA	TTTCACCATC	840
TGCTTCCCCC	CCACCAAGNN	NNNNGATATC	TGGGAAGACG	TACATGCTTG	GCTGACTTGT	900
GCATGGCACC	ATCAGCTCAA	TTTTTAATTT	TTTAATTTTA	ATTTAATTTA	ATTTTATGTT	960
TTTGAGACAG	AGCCTCACTG	TGTAGTCCTG	GCTGGCCTGG	CTGGTTCTCT	ATTTAGACCA	1020
GGTTAGCCTT	GAAGTCACAG	AGATCTGCCT	GCTTCTGCCT	CCCAAGTGCT	GGGTTCAACC	1080
AGGTCTGGCA	AGCGCTCCAT	TTTTCAGCTC	CTCTGCAACA	GTGC		1124

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: variant
- (B) LOCATION: 5, 386, 394
- (D) OTHER INFORMATION: Xaa = any amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr	Leu	Tyr	Thr	Xaa	Gln	His	Pro	Val	Ala	Gly	Ser	Gln	Asp	Ile	Lys
1				5					10					15	
Met	Lys	Ile	Leu	Ile	Leu	Val	Ala	Ala	Gly	Leu	Leu	Phe	Leu	Pro	Val
			20					25					30		
Thr	Val	Cys	Gln	Ser	Gly	Ile	Asn	Val	Ser	Asp	Asn	Ser	Ala	Lys	Pro
		35					40					45			
Thr	Leu	Thr	Ile	Lys	Ser	Phe	Asn	Gly	Gly	Pro	Gln	Asn	Thr	Phe	Glu
	50					55					60				
Glu	Phe	Pro	Leu	Ser	Asp	Ile	Glu	Gly	Trp	Thr	Gly	Ala	Thr	Thr	Thr
65					70					75					80
Ile	Lys	Ala	Glu	Cys	Pro	Glu	Asp	Ser	Ile	Ser	Thr	Leu	His	Val	Asn
				85					90					95	
Asn	Ala	Thr	Ile	Gly	Tyr	Leu	Arg	Ser	Ser	Leu	Ser	Thr	Gln	Val	Ile
		100						105					110		
Pro	Ala	Ile	Tyr	Ile	Leu	Leu	Phe	Val	Val	Gly	Val	Pro	Ser	Asn	Ile
		115					120					125			
Val	Thr	Leu	Trp	Lys	Leu	Ser	Leu	Arg	Thr	Lys	Ser	Ile	Ser	Leu	Val
	130					135					140				
Ile	Phe	His	Thr	Asn	Leu	Ala	Ile	Ala	Asp	Leu	Leu	Phe	Cys	Val	Thr
145					150					155					160
Leu	Pro	Phe	Lys	Ile	Ala	Tyr	His	Leu	Asn	Gly	Asn	Asn	Trp	Val	Phe
				165					170					175	
Gly	Glu	Val	Met	Cys	Arg	Ile	Thr	Thr	Val	Val	Phe	Tyr	Gly	Asn	Met
		180						185					190		
Tyr	Cys	Ala	Ile	Leu	Ile	Leu	Thr	Cys	Met	Gly	Ile	Asn	Arg	Tyr	Leu
		195					200					205			
Ala	Thr	Ala	His	Pro	Phe	Thr	Tyr	Gln	Lys	Leu	Pro	Lys	Arg	Ser	Phe
	210						215					220			
Ser	Leu	Leu	Met	Cys	Gly	Ile	Val	Trp	Val	Met	Val	Phe	Leu	Tyr	Met
225					230					235					240

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAGGCATGG	AAAATGATAC	AAACAACCTTG	GCAAAGCCAA	CCTTACCCAT	TAAGACCTTT	60
CGTGGAGCTC	CCCCAAATTC	TTTTGAAGAG	TTCCCCTTTT	CTGCCCTGGA	AGGCTGGACA	120
GGAGCCACGA	TTACTGTAAA	AATTAAGTGC	CCTGAAGAAA	GTGCTTCACA	TCTCCATGTG	180
AAAAATGCTA	CCATGGGGTA	CCTGACCAGC	TCCTTAAGTA	CTAAACTGAT	ACCTGCCATC	240
TACCTCCTGG	TGTTTGTAGT	TGGTGTCCCG	GCCAATGCTG	TGACCCTGTG	GATGCTTTTC	300
TTCAGGACCA	GATCCATCTG	TACCACTGTA	TTCTACACCA	ACCTGGCCAT	TGCAGATTTT	360
CTTTTTTTGTG	TTACATTGCC	CTTTAAGATA	GCTTATCATC	TCAATGGGAA	CAACTGGGTA	420
TTTGGAGAGG	TCCTGTGCCG	GGCCACCACA	GTCATCTTCT	ATGGCAACAT	GTA CTGCTCC	480
ATTCTGCTCC	TTGCCTGCAT	CAGCATCAAC	CGCTACCTGG	CCATCGTCCA	TCCTTTCACC	540
TACCGGGGCC	TGCCCAAGCA	CACCTATGCC	TTGGTAACAT	GTGGACTGGT	GTGGGCAACA	600
GTTTTCTTAT	ATATGCTGCC	ATTTTTCATA	CTGAAGCAGG	AATATTATCT	TGTTTCAGCCA	660
GACATCACCA	CCTGCCATGA	TGTTCAACAAC	ACTTGCGAGT	CCTCATCTCC	CTTCCAACCTC	720
TATTACTTCA	TCTCCTTGGC	ATTCTTTGGA	TTCTTAATTC	CATTTGTGCT	TATCATCTAC	780
TGCTATGCAG	CCATCATCCG	GACACTTAAT	GCATACGATC	ATAGATGGTT	GTGGTATGTT	840
AAGGCGAGTC	TCCTCATCCT	TGTGATTTTT	ACCATTTGCT	TTGCTCCAAG	CAATATTATT	900
CTTATTATTCT	ACCATGCTAA	CTACTACTAC	AACAACACTG	ATGGCTTATA	TTTTATATAT	960
CTCATAGCTT	TGTGCCTGGG	TAGTCTTAAT	AGTTGCTTAG	ATCCATTCCCT	TTATTTTCTC	1020
ATGTCAAAAA	CCAGAAATCA	CTCCACTGCT	TACCTTACAA	AATAGTGAAA	TGATCTTAGA	1080
GAACAAGGAC	AGCCATCACA	GA				1102

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: variant
- (B) LOCATION: 9, 394, 395
- (D) OTHER INFORMATION: Xaa = any amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys	Ser	Met	Ile	Leu	Gln	Ile	Ser	Xaa	Arg	Leu	Arg	Asp	Gly	Thr	Gln	
1				5				10					15			
Val	Ile	Lys	Met	Lys	Ala	Leu	Ile	Phe	Ala	Ala	Ala	Gly	Leu	Leu	Leu	
			20					25					30			
Leu	Leu	Pro	Thr	Phe	Cys	Gln	Ser	Gly	Met	Glu	Asn	Asp	Thr	Asn	Asn	
			35					40					45			
Leu	Ala	Lys	Pro	Thr	Leu	Pro	Ile	Lys	Thr	Phe	Arg	Gly	Ala	Pro	Pro	
			50					55					60			
Asn	Ser	Phe	Glu	Glu	Phe	Pro	Phe	Ser	Ala	Leu	Glu	Gly	Trp	Thr	Gly	
65					70					75					80	

Ala	Thr	Ile	Thr	Val	Lys	Ile	Lys	Cys	Pro	Glu	Glu	Ser	Ala	Ser	His
				85					90					95	
Leu	His	Val	Lys	Asn	Ala	Thr	Met	Gly	Tyr	Leu	Thr	Ser	Ser	Leu	Ser
			100					105					110		
Thr	Lys	Leu	Ile	Pro	Ala	Ile	Tyr	Leu	Leu	Val	Phe	Val	Val	Gly	Val
		115					120					125			
Pro	Ala	Asn	Ala	Val	Thr	Leu	Trp	Met	Leu	Phe	Phe	Arg	Thr	Arg	Ser
	130					135					140				
Ile	Cys	Thr	Thr	Val	Phe	Tyr	Thr	Asn	Leu	Ala	Ile	Ala	Asp	Phe	Leu
145					150					155					160
Phe	Cys	Val	Thr	Leu	Pro	Phe	Lys	Ile	Ala	Tyr	His	Leu	Asn	Gly	Asn
				165					170					175	
Asn	Trp	Val	Phe	Gly	Glu	Val	Leu	Cys	Arg	Ala	Thr	Thr	Val	Ile	Phe
			180					185					190		
Tyr	Gly	Asn	Met	Tyr	Cys	Ser	Ile	Leu	Leu	Leu	Ala	Cys	Ile	Ser	Ile
		195					200					205			
Asn	Arg	Tyr	Leu	Ala	Ile	Val	His	Pro	Phe	Thr	Tyr	Arg	Gly	Leu	Pro
	210					215					220				
Lys	His	Thr	Tyr	Ala	Leu	Val	Thr	Cys	Gly	Leu	Val	Trp	Ala	Thr	Val
225					230					235					240
Phe	Leu	Tyr	Met	Leu	Pro	Phe	Phe	Ile	Leu	Lys	Gln	Glu	Tyr	Tyr	Leu
				245					250					255	
Val	Gln	Pro	Asp	Ile	Thr	Thr	Cys	His	Asp	Val	His	Asn	Thr	Cys	Glu
			260					265					270		
Ser	Ser	Ser	Pro	Phe	Gln	Leu	Tyr	Tyr	Phe	Ile	Ser	Leu	Ala	Phe	Phe
		275					280					285			
Gly	Phe	Leu	Ile	Pro	Phe	Val	Leu	Ile	Ile	Tyr	Cys	Tyr	Ala	Ala	Ile
	290					295					300				
Ile	Arg	Thr	Leu	Asn	Ala	Tyr	Asp	His	Arg	Trp	Leu	Trp	Tyr	Val	Lys
305				310					315						320
Ala	Ser	Leu	Leu	Ile	Leu	Val	Ile	Phe	Thr	Ile	Cys	Phe	Ala	Pro	Ser
				325					330					335	
Asn	Ile	Ile	Leu	Ile	Ile	His	His	Ala	Asn	Tyr	Tyr	Tyr	Asn	Asn	Thr
			340					345					350		
Asp	Gly	Leu	Tyr	Phe	Ile	Tyr	Leu	Ile	Ala	Leu	Cys	Leu	Gly	Ser	Leu
		355					360					365			
Asn	Ser	Cys	Leu	Asp	Pro	Phe	Leu	Tyr	Phe	Leu	Met	Ser	Lys	Thr	Arg
	370					375					380				
Asn	His	Ser	Thr	Ala	Tyr	Leu	Thr	Lys	Xaa	Xaa	Asn	Asp	Leu	Arg	Glu
385					390					395					400
Gln	Gly	Gln	Pro	Ser	Gln	Arg	Thr								
					405										

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Gly	Pro	Arg	Arg	Leu	Leu	Leu	Val	Ala	Ala	Cys	Phe	Ser	Leu	Cys
1				5				10						15	

Gly	Pro	Leu	Leu	Ser	Ala	Arg	Thr	Arg	Ala	Arg	Arg	Pro	Glu	Ser	Lys			
			20					25					30					
Ala	Thr	Asn	Ala	Thr	Leu	Asp	Pro	Arg	Ser	Phe	Leu	Leu	Arg	Asn	Pro			
		35					40					45						
Asn	Asp	Lys	Tyr	Glu	Pro	Phe	Trp	Glu	Asp	Glu	Glu	Lys	Asn	Glu	Ser			
	50					55					60							
Gly	Leu	Thr	Glu	Tyr	Arg	Leu	Val	Ser	Ile	Asn	Lys	Ser	Ser	Pro	Leu			
65					70					75					80			
Gln	Lys	Gln	Leu	Pro	Ala	Phe	Ile	Ser	Glu	Asp	Ala	Ser	Gly	Tyr	Leu			
				85					90					95				
Thr	Ser	Ser	Trp	Leu	Thr	Leu	Phe	Val	Pro	Ser	Val	Tyr	Thr	Gly	Val			
			100					105					110					
Phe	Val	Val	Ser	Leu	Pro	Leu	Asn	Ile	Met	Ala	Ile	Val	Val	Phe	Ile			
			115				120					125						
Leu	Lys	Met	Lys	Val	Lys	Lys	Pro	Ala	Val	Val	Tyr	Met	Leu	His	Leu			
	130					135					140							
Ala	Thr	Ala	Asp	Val	Leu	Phe	Val	Ser	Val	Leu	Pro	Phe	Lys	Ile	Ser			
145					150					155					160			
Tyr	Tyr	Phe	Ser	Gly	Ser	Asp	Trp	Gln	Phe	Gly	Ser	Glu	Leu	Cys	Arg			
				165				170						175				
Phe	Val	Thr	Ala	Ala	Phe	Tyr	Cys	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu			
			180				185						190					
Met	Thr	Val	Ile	Ser	Ile	Asp	Arg	Phe	Leu	Ala	Val	Val	Tyr	Pro	Met			
		195				200						205						
Gln	Ser	Leu	Ser	Trp	Arg	Thr	Leu	Gly	Arg	Ala	Ser	Phe	Thr	Cys	Leu			
	210					215					220							
Ala	Ile	Trp	Ala	Leu	Ala	Ile	Ala	Gly	Val	Val	Pro	Leu	Val	Leu	Lys			
225					230					235					240			
Glu	Gln	Thr	Ile	Gln	Val	Pro	Gly	Leu	Asn	Ile	Thr	Thr	Cys	His	Asp			
				245					250					255				
Val	Leu	Asn	Glu	Thr	Leu	Leu	Glu	Gly	Tyr	Tyr	Ala	Tyr	Tyr	Phe	Ser			
			260				265						270					
Ala	Phe	Ser	Ala	Val	Phe	Phe	Phe	Val	Pro	Leu	Ile	Ile	Ser	Thr	Val			
			275				280					285						
Cys	Tyr	Val	Ser	Ile	Ile	Arg	Cys	Leu	Ser	Ser	Ser	Ala	Val	Ala	Asn			
	290					295				300								
Arg	Ser	Lys	Lys	Ser	Arg	Ala	Leu	Phe	Leu	Ser	Ala	Ala	Val	Phe	Cys			
305					310					315					320			
Ile	Phe	Ile	Ile	Cys	Phe	Gly	Pro	Thr	Asn	Val	Leu	Leu	Ile	Ala	His			
				325					330					335				
Tyr	Ser	Phe	Leu	Ser	His	Thr	Ser	Thr	Thr	Glu	Ala	Ala	Tyr	Phe	Ala			
			340				345						350					
Tyr	Leu	Leu	Cys	Val	Cys	Val	Ser	Ser	Ile	Ser	Ser	Cys	Ile	Asp	Pro			
		355				360						365						
Leu	Ile	Tyr	Tyr	Tyr	Ala	Ser	Ser	Glu	Cys	Gln	Arg	Tyr	Val	Tyr	Ser			
	370					375					380							
Ile	Leu	Cys	Cys	Lys	Glu	Ser	Ser	Asp	Pro	Ser	Ser	Tyr	Asn	Ser	Ser			
385					390					395					400			
Gly	Gln	Leu	Met	Ala	Ser	Lys	Met	Asp	Thr	Cys	Ser	Ser	Asn	Leu	Asn			
				405				410						415				
Asn	Ser	Ile	Tyr	Lys	Lys	Leu	Leu	Thr										
			420				425											

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Arg	Ser	Pro	Ser	Ala	Ala	Trp	Leu	Leu	Gly	Ala	Ala	Ile	Leu	Leu
1				5				10					15		
Ala	Ala	Ser	Leu	Ser	Cys	Ser	Gly	Thr	Ile	Gln	Gly	Thr	Asn	Arg	Ser
			20					25					30		
Ser	Lys	Gly	Arg	Ser	Leu	Ile	Gly	Lys	Val	Asp	Gly	Thr	Ser	His	Val
		35					40					45			
Thr	Gly	Lys	Gly	Val	Thr	Val	Glu	Thr	Val	Phe	Ser	Val	Asp	Glu	Phe
	50					55				60					
Ser	Ala	Ser	Val	Leu	Thr	Gly	Lys	Leu	Thr	Thr	Val	Phe	Leu	Pro	Ile
65					70					75					80
Val	Tyr	Thr	Ile	Val	Phe	Val	Val	Gly	Leu	Pro	Ser	Asn	Gly	Met	Ala
				85					90					95	
Leu	Trp	Val	Phe	Leu	Phe	Arg	Thr	Lys	Lys	Lys	His	Pro	Ala	Val	Ile
			100					105					110		
Tyr	Met	Ala	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Ser	Val	Ile	Trp	Phe
	115						120					125			
Pro	Leu	Lys	Ile	Ala	Tyr	His	Ile	His	Gly	Asn	Asn	Trp	Ile	Tyr	Gly
	130					135					140				
Glu	Ala	Leu	Cys	Asn	Val	Leu	Ile	Gly	Phe	Phe	Tyr	Gly	Asn	Met	Tyr
145					150					155					160
Cys	Ser	Ile	Leu	Phe	Met	Thr	Cys	Leu	Ser	Val	Gln	Arg	Tyr	Trp	Val
				165					170					175	
Ile	Val	Asn	Pro	Met	Gly	His	Ser	Arg	Lys	Lys	Ala	Asn	Ile	Ala	Ile
			180					185					190		
Gly	Ile	Ser	Leu	Ala	Ile	Trp	Leu	Leu	Ile	Leu	Leu	Val	Thr	Ile	Pro
	195						200					205			
Leu	Tyr	Val	Val	Lys	Gln	Thr	Ile	Phe	Ile	Pro	Ala	Leu	Asn	Ile	Thr
	210					215					220				
Thr	Cys	His	Asp	Val	Leu	Pro	Glu	Gln	Leu	Leu	Val	Gly	Asp	Pro	Phe
225					230					235					240
Leu	Ser	Leu	Ala	Ile	Gly	Val	Phe	Leu	Phe	Pro	Ala	Phe	Leu	Thr	Ala
			245					250						255	
Ser	Ala	Tyr	Val	Leu	Met	Ile	Arg	Met	Leu	Arg	Ser	Ser	Ala	Met	Asp
		260					265						270		
Glu	Asn	Ser	Glu	Lys	Lys	Arg	Lys	Arg	Ala	Ile	Lys	Leu	Ile	Val	Thr
	275						280					285			
Val	Leu	Ala	Met	Tyr	Leu	Ile	Cys	Phe	Thr	Pro	Ser	Asn	Leu	Leu	Leu
	290					295					300				
Val	Val	His	Tyr	Phe	Leu	Ile	Lys	Ser	Gln	Gly	Gln	Ser	His	Val	Tyr
305					310					315					320
Ala	Leu	Tyr	Ile	Val	Ala	Leu	Cys	Leu	Ser	Thr	Leu	Asn	Ser	Cys	Ile
			325					330						335	
Asp	Pro	Phe	Val	Tyr	Tyr	Phe	Val	Ser	His	Asp	Phe	Arg	Asp	His	Ala
		340					345						350		
Lys	Asn	Ala	Leu	Leu	Cys	Arg	Ser	Val	Arg	Thr	Val	Lys	Gln	Met	Gln
	355						360					365			
Val	Ser	Leu	Thr	Ser	Lys	Lys	His	Ser	Arg	Lys	Ser	Ser	Ser	Tyr	Ser
	370					375					380				
Ser	Ser	Ser	Thr	Thr	Val	Lys	Thr	Ser	Tyr						

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Phe Glu Glu Ile Pro Glu Glu Tyr Leu Gln
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ix), FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...29
(D) OTHER INFORMATION: N=Inosine at residues 3, 12, 18, 21, and 24

- (A) NAME/KEY: Other
(B) LOCATION: 22...27
(D) OTHER INFORMATION: N= A, T, C, or G at residues 22 and 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTNTACATGC TNMACYTNGC NNTNGCNGA.

29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 6...21
(D) OTHER INFORMATION: N= Inosine at residues 6, 9, 12, 15, and 21

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 24
- (D) OTHER INFORMATION: B= C, G, or T at residue 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGATANACNA CNGCNADRWA NCKBTC

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Tyr Lys Asp Asp Asp
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Ser Lys Gly Ser Ser Gln Lys Gly Ser Arg Leu Leu Leu Leu
1 5 10 15
Leu Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr
20 25 30
Lys Asp Asp Asp Asp Val Glu
35

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Phe Glu Glu Phe Pro
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Thr Pro Lys

1

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Phe Arg Gly Ala Pro

1

5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Phe Arg Gly Ala Pro Pro Asn Ser

1

5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Pro Ile Lys Thr Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Xaa Pro Arg Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu Phe
1 5 10 15
Pro Phe Ser Ala Leu Glu
20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Pro Ile Lys
1

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Thr Phe Arg Gly Ala Pro Pro Asn Ser
1 5